```
   1  GCCAGCATTCGGCACGAGGGGGTAGGACCCTCCGAGCCAGGTGTGGATATAGTCTCGTGGTGCGCCGTTTTTAAGCCG        80
  81  GTCTGAAAAGCGCCAATATTCGGGTGGGAGTGACCCGATTTTCCAGGCTGCTATCCATGTCCAGGGCCAAACATGAATCCT    160
 161  ATTGCTCTTGGGAGCCGCTGCTTATGCTGCTTAGTCGTTGATGTCATCAGTCCCGTGGTGGAGCCTGTGG               240
 241  AGACAACATTCAGTCTTATACTGCCACAGTCATTAGTGTCTAAAACATTGAAAAGTGGCTGACAATGTAGGGAAAG         320
 321  TGGTGACTCAGCTGACAGGCACACTGCCTTCAGGTGTGATGACAGAGAGATGATGTTGCCATCCACAGTAATTCACGGCCGGAGT  400
 401  CCTTTGGTCCCAGGCATCATCACAGTTATTGACACCGAAACCGTTGGAGAGGGCCAGGTGCTTGTGAGTGAGGATTCTGA     480
 481  CAGTGATGGCATTGTGCCCACTCCCTGCCCATGAGAAGCCAGGTGCTGCATGGCTTTTAATACAAGTGAATGCTTC         560
 561  TAGTCACAACAGACACCCTTGGCCATGACTTTCATGTCTTCCAAATTCGACTCATCCTTGTCTCCATCACAATGTGCT       640
 641  GTCCACCATCTGTATACTCTTCACAGGGGAGAAACTGAAGCCAAGTACAGGACATCGCTTCAGCCATGACTGTCGCTG       720
 721  GGTTGTGGTCAGTACTCTCCGGGGTACTTCCCGGTTTCCCATCAACCCTTATGGTGGCCAGCCTTGTTGTTGTACAC        800
 801  ATATGTGTCACCGAGTAGTGAATGCATGAGCCGGTTCCCAGAAAAGTGCTGGACTGGAAGAGATTGAACAAGAACTGACG     880
 881  TCTAAGCAAGGAGTCGCGTGTAGCCCCTGTTCCAGGTCTCTATCAAGAGCCCCTTCGTGGGTCGCTGTCCGGAAACTGAA    960
 961  CAGCCAAGACTCCTATAAACAATTTTACCAACAACAACCCTGGCAACATGGGACCATCCAAAACGAACCGGGCCTTATCTCTTTGGAGCG  1040
1041  TGATGCCTCTTGCACAAATCAAGCAGCCAATGACAATTGGGACCAATGCAAAGTTAAACCTCCTCCACAAATTCACCCAGCAAATTGATGGGCGGAGAATT  1120
1121  GGGTGTTTTCCATAAAGCCCATGCTGTAGCCTGTGGCCTTAATCTTTGATGGTAG                              1200
1201  TTGTGTGGCCTCATCTTCCGAACATCCAGGTCATGGTTTGCAAATAATGCAGGTCTGAAATAATGCAGTCAGTCCA         1280
```

FIG. 1A

```
        1  AACAAGTTGTAGTTGAGTCCCGTACATTATCAGTTGCTATGGCACCTTAGTGAACACATGATGGAGCCGCGACCCTC         0
     1281                                                                             1360

        1  AGCACTGCACCCAAGATTAGTGACGACACACCACTGGAAATGACATGCGCCTCCGAGCCAGCTGGACTCTGGTTAGAAC       0
     1361                                                                             1440

        1  CCCTCAATGAATGAATTGCAGCCACCGTTTAATGCAAACCACCCCTGCTCCTCGCCAGATGCAGTACAGTATTATC        0
     1441                                                                             1520

        1  AGTTCCGTCGTGCCTGGCCTGGTTCCCCCTGGAAGTCCTCGGGCCCATTACTCGACATGGGTCTTACGACAGTTTAGCTTCT   0
     1521                                                                             1600

        1  GACCATAGTGGACAGGAAGGATGAAGAAATGGCTTTCCCAGGTTGAAATTGTAACACACTGACCCCATAGACGTCTGTG      0
     1601                                                                             1680

        1  GATGGGTCCACAGTTCCAGTTCAAAAACCATCCATCCCTCAGGCCAAACCACAGTTATCTCATCCAGTTCATCTGTGTTGC    0
     1681                                                                             1760

        1  AGTCTCATGTCCGAGTGACACGCCACAGCCCTCTTTTGGATTTGATACAGATGATCTTGATCTCAACAGTCTCAGGATC      0
     1761                                                                             1840

        1                            TCGGAGCCCATGCCGCAGCGGGGCGGTTAGCTCGCCCTCTTCCTGACCCC                 50
     1841  CAGCCAGTCCGCCGCTCCTGACCCCGTCGCATGCCGTCCAGTCCGTCCAGTCTCTGATCGAAGGGGAGTTTCCACAGTGAT   1920
                                    **  *   *  *   *    *       *          *   *   *  *

       51  CGATCCTGGGCCGAGTACCTTTGACAGGAGCGGTACCCTGCTGGAGCGTGTGCGAGGCTTCGGGGCT               130
     1921  TGATGCTG--CCTCAGTGACCTTTGACAGGAGCAGCAGCGGTACCCTGCTGGAGCGTGTGCGAGGCTTCGGGGCT         1998
            *** ***   *  *******************************************************

      131  GCGGCACATGTCCTCCATGGAGCGACACGGAGGAGGGCCTCCGGGAGCCATTGCCGACGCCATGGCCGAGTCACCTAGCC    210
     1999  GCGGCACATGTCCTCCATGGAGCGACACGGAGGAGGGCTCCGGGAGCCATTGCCGACGCCATGGCCGAGTCACCTAGCC    2078
            *****************************************************************

      211  GGGAGCGTCGTGTGGGATCCGGAACAGAACTTCAGCGAGAGGAAGCATCGAGACTTCGAGTAACAGCTCAGGCTCCACCAGC    290
     2079  GG-ACGTCGTGGGGATCCGGAACAGAGGAGGAAGCAGAGGAAAAAAAAAAAGG  SEQ.ID NO:317    2124
            *********************  ***  *  *     *   **   **

      291  GGCAGCATACCAAGAAACTTTGATGGCTACCAGCAACCTGCTTCTGACTGGCCAG  412  SEQ.ID NO:315    370
     2125                                                             2124

      371  TGGCTTCCCGTAGTACCAGCAACCTGCTTCTGACTGGCCAG  412    SEQ.ID NO:315
     2125                                                 2124
```

FIG. 1B

```
1     CGAGAACTCTGAGTAACAGCTCAGGCTCCACCAGGGGCAGCATACCAAGAAACTTTGATGGCTACCGATCTCCGGCTGCCC      0
1                                                                                           80

1                GCCAGCCCCTCAGCCTCTTCCCGACTGGCTTCCCGGTAGTACCAGCAACCTGCTTCTGACTGGCCAGCCC       70
81    ACCAATGAGAGCCAGCCCCTCAGCCTCTTCCCGACTGGCTTCCCGGTAGTACCAGCAACCTGCTTCTGACTGGCCAGCCC      160
                 ********************************************************************

71    CCTCCCCTGCTGGAGGAGGGGAGAAGCCCCGCTCTGTCCTACCCTTCAGTCTCTTCCTTCATCAACCACCTTCC           150
161   CCTCCCCTGCTGGAGGAGGGGAGAAGCCCCGCTCTGTCCTACCCTTCAGTCTCTTCCTTCATCAACCACCTTCC           240
      *************************************************************************

151   CCAAGCTTAGTGACAGCAGCCGCGCCATCCTACCTGGATGGAGAAGAGACCCTTCTCCAAGCACCTCAGCGCACTTGCCCT     230
241   CCAAGCTTAGTGACAGCAGCCGCGCCATCCTACCTGGATGGAGAAGAGACCCTTCTCCAAGCACCTCAGCGCACTTGCCCT     320
      **********************************************************************************

231   CTGCCACACCGTCGGTGGGGAGGCTGTGTGGCCAGGAGAGAGACTGTAGAAGCTCGGTCCCGTCCCGTGTATGTTTGCA     SEQ. ID NO:316  300
321   CTGCCACACCGTCGGTGGGGAGGCTGTGTGGCCAGGAGAGAGACTGTAGAAGCTCGGTCCCGTGTATGTTTGCATATGACATCC             400
      **********************************************************************

301   TGCATTGGATCCGCTTTTGTATTTTTAACCATACCCAGGTGGGGGGGTGGGGAGCCTGGAACAGTGACCAGATCT           300
401                                                                                       480

301   GGGGGCCTGATGGGGGACAGAGTTGATCGTCCACCTGGCCCATTTGACCCTGAGTGACAGTCACAGCCTCAGCTCATGT       300
481                                                                                       560

301   CTGGCTGTGACACACTGCCCCCAGCTTCCCTTGGTCAGCCCCACTCCAGCACGGGGTGAACGGAGCCCAGAGTACTA        300
561                                                                                       640

301   GGGAAGGAGGAAGGGAGGGACATGCCTCTTCTTCTTCCCATCTGTTCTTCCGGAAGAGTTTGTCTTTCTTAT            300
641                                                                                       720

301   CTTTAAGCCCCTTTACCCTGGTCCTGTACTCGTGTACTGATCAGTGAAGGAGAAACCGTGGTTACTGAGGCCCTGTTGAAAAGTGCACGT     300
721                                                                                       800

301   CTTGTCCAATAAATCACGCTGCCAGTTGGAAAAAAAAAAAGGATCTTTAATTAAGCGGCCGCAAGCTTATT            300
801                                                                                       880

301   CCCTTTAGTGAGGGTTAATTTAGCTTGGCACTGCCGTCGTTTACAAGTCGTGACTGGTAAACCCTGGCGTTACCCA          300
881                                                                                       960

301   ACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAAC     300
961                                                                                       1040

301   AGTTGCGCAGCCTGAATGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACCGCGCAG     300
1041                                                                                      1120

301   CGTTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGC     300
1121                                                                                      1200

301   TTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAA        300
1201                                                                                      1280

301   AACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCAC     300
1281                                                                                      1360

301   GTTCT    1365
1361
```

SEQ. ID NO:318

FIG.2